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PASSWORD:
TERMINAL (ENTER 1, 2, 3, OR ?):2

* * * * * * * * *   Welcome to STN International   * * * * * * * * * *

NEWS 1   Web Page URLs for STN Seminar Schedule - N. America
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NEWS 3   DEC 05 CASREACT(R) - Over 10 million reactions available
NEWS 4   DEC 14 2006 MeSH terms loaded in MEDLINE/LMEDLINE
NEWS 5   DEC 14 2006 MeSH terms loaded for MEDLINE file segment of TOXCENTER
NEWS 6   DEC 14 CA/CAplus to be enhanced with updated IPC codes
NEWS 7   DEC 21 IPC search and display fields enhanced in CA/CAplus with the
                  IPC reform
NEWS 8   DEC 23 New IPC8 SEARCH, DISPLAY, and SELECT fields in USPATFULL/
                  USPAT2
NEWS 9   JAN 13 IPC 8 searching in IFIPAT, IFIUDB, and IFICDB
NEWS 10   JAN 13 New IPC 8 SEARCH, DISPLAY, and SELECT enhancements added to
                  INPADOC
NEWS 11   JAN 17 Pre-1988 INPI data added to MARPAT
NEWS 12   JAN 17 IPC 8 in the WPI family of databases including WPIFV
NEWS 13   JAN 30 Saved answer limit increased
NEWS 14   JAN 31 Monthly current-awareness alert (SDI) frequency
                  added to TULSA

NEWS EXPRESS   JANUARY 03 CURRENT VERSION FOR WINDOWS IS V8.01,
                  CURRENT MACINTOSH VERSION IS V6.0c(ENG) AND V6.0Jc(JP),
                  AND CURRENT DISCOVER FILE IS DATED 19 DECEMBER 2005.
                  V8.0 USERS CAN OBTAIN THE UPGRADE TO V8.01 AT
                  http://download.cas.org/express/v8.0-Discover/

NEWS HOURS   STN Operating Hours Plus Help Desk Availability
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  agreement. Please note that this agreement limits use to scientific
  research. Use for software development or design or implementation
  of commercial gateways or other similar uses is prohibited and may
  result in loss of user privileges and other penalties.

  * * * * * * * * * * * * * STN Columbus * * * * * * * * * * * * * * * * *

FILE 'HOME' ENTERED AT 17:18:39 ON 09 FEB 2006

=> FIL CAPLUS
COST IN U.S. DOLLARS   SINCE FILE   TOTAL
                                                    ENTRY   SESSION
FULL ESTIMATED COST   0.21   0.21

FILE 'CAPLUS' ENTERED AT 17:18:49 ON 09 FEB 2006
USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.
PLEASE SEE "HELP USAGETERMS" FOR DETAILS.

FILE COVERS 1907 - 9 Feb 2006 VOL 144 ISS 7
FILE LAST UPDATED: 8 Feb 2006 (20060208/ED)

Effective October 17, 2005, revised CAS Information Use Policies apply.
They are available for your review at:

http://www.cas.org/infopolicy.html

=> s tgtagcggcccacgctgg/sqsn
   REG1stRY INITIATED
Substance data SEARCH and crossover from CAS REGISTRY in progress...
Use DISPLAY HITSTR (or FHITSTR) to directly view retrieved structures.

L2   0 L1

=> s taccacgcgacacacttc/sqsn
   REG1stRY INITIATED
Substance data SEARCH and crossover from CAS REGISTRY in progress...
Use DISPLAY HITSTR (or FHITSTR) to directly view retrieved structures.

L4   1 L3

=> d l4

L4   ANSWER 1 OF 1 CAPLUS COPYRIGHT 2006 ACS on STN
AN   2002:10074 CAPLUS
DN   136:65204
TI   Transgenic corn plant PV-ZMGT32 (nk603) transformed with DNA construct
      containing 5-enolpyruvoylshikimate 3-phosphate synthase for conferring
      glyphosate tolerance
IN   Behr, Carl F.; Hironaka, Catherine; Heck, Gregory R.; You, Jinsong
PA   Monsanto Technology Llc, USA
SO   Eur. Pat. Appl., 25 pp.
      CODEN: EPXXDW
DT   Patent
LA   English
FAN.CNT 1
      PATENT NO.   KIND   DATE   APPLICATION NO.   DATE
      ---------------   ----   -------- --------------------   --------
PI   EP 1167531   A1   20020102 EP 2001-202314   20010615
          R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
              IE, SI, LT, LV, FI, RO
      BR 2001000752   A   20020213 BR 2001-752   20010222
      ZA 2001004092   A   20011119 ZA 2001-4092   20010518
      US 2002013960   A1   20020131 US 2001-872051   20010601

```
        US 6825400              B2     20041130
        EP 1582592              A1     20051005    EP 2005-105879           20010615
           R:  AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
               IE, SI, LT, LV, FI, RO, MK, CY, AL, TR
        CA 2349841              AA     20011222    CA 2001-2349841          20010620
        CN 1332246              A      20020123    CN 2001-122036           20010622
        BG 105637               A      20020430    BG 2001-105637           20010622
        US 2004139493           A1     20040715    US 2004-790430           20040301
PRAI US 2000-213567P            P      20000622
     US 2000-240014P            P      20001013
     US 2000-241215P            P      20001013
     US 2001-872051             A3     20010601
     EP 2001-202314             A3     20010615
RE.CNT  3       THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD
                ALL CITATIONS AVAILABLE IN THE RE FORMAT


=> s accaagcttttataatag/sqsn
   REG1stRY INITIATED
Substance data SEARCH and crossover from CAS REGISTRY in progress...
Use DISPLAY HITSTR (or FHITSTR) to directly view retrieved structures.




L6              1 L5

=> d 16

L6   ANSWER 1 OF 1   CAPLUS   COPYRIGHT 2006 ACS on STN
AN   2002:10074   CAPLUS
DN   136:65204
TI   Transgenic corn plant PV-ZMGT32 (nk603) transformed with DNA construct
     containing 5-enolpyruvoylshikimate 3-phosphate synthase for conferring
     glyphosate tolerance
IN   Behr, Carl F.; Hironaka, Catherine; Heck, Gregory R.; You, Jinsong
PA   Monsanto Technology Llc, USA
SO   Eur. Pat. Appl., 25 pp.
     CODEN: EPXXDW
DT   Patent
LA   English
FAN.CNT 1
     PATENT NO.              KIND   DATE        APPLICATION NO.          DATE
     ---------------         ----   --------    ---------------------    --------
PI   EP 1167531              A1     20020102    EP 2001-202314           20010615
        R:  AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
            IE, SI, LT, LV, FI, RO
        BR 2001000752           A      20020213    BR 2001-752              20010222
        ZA 2001004092           A      20011119    ZA 2001-4092             20010518
        US 2002013960           A1     20020131    US 2001-872051           20010601
        US 6825400              B2     20041130
        EP 1582592              A1     20051005    EP 2005-105879           20010615
           R:  AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
               IE, SI, LT, LV, FI, RO, MK, CY, AL, TR
        CA 2349841              AA     20011222    CA 2001-2349841          20010620
        CN 1332246              A      20020123    CN 2001-122036           20010622
        BG 105637               A      20020430    BG 2001-105637           20010622
        US 2004139493           A1     20040715    US 2004-790430           20040301
PRAI US 2000-213567P            P      20000622
     US 2000-240014P            P      20001013
     US 2000-241215P            P      20001013
     US 2001-872051             A3     20010601
     EP 2001-202314             A3     20010615
RE.CNT  3       THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD
                ALL CITATIONS AVAILABLE IN THE RE FORMAT
```

```
=> d his

        (FILE 'HOME' ENTERED AT 17:18:39 ON 09 FEB 2006)

        FILE 'CAPLUS' ENTERED AT 17:18:49 ON 09 FEB 2006
                    S TGTAGCGGCCCACGCTGG/SQSN

        FILE 'REGISTRY' ENTERED AT 17:19:17 ON 09 FEB 2006
L1                0 S TGTAGCGGCCCACGCTGG/SQSN

        FILE 'CAPLUS' ENTERED AT 17:19:37 ON 09 FEB 2006
L2                0 S L1
                    S TACCACGCGACACACTTC/SQSN

        FILE 'REGISTRY' ENTERED AT 17:20:40 ON 09 FEB 2006
L3                6 S TACCACGCGACACACTTC/SQSN

        FILE 'CAPLUS' ENTERED AT 17:21:00 ON 09 FEB 2006
L4                1 S L3
                    S ACCAAGCTTTTATAATAG/SQSN

        FILE 'REGISTRY' ENTERED AT 17:22:13 ON 09 FEB 2006
L5                8 S ACCAAGCTTTTATAATAG/SQSN

        FILE 'CAPLUS' ENTERED AT 17:22:35 ON 09 FEB 2006
L6                1 S L5
```

NCBI   results of **BLAST**

BLASTN 2.2.13 [Nov-27-2005]

Reference:
Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman
(1997), "Gapped BLAST and PSI-BLAST: a new generation of
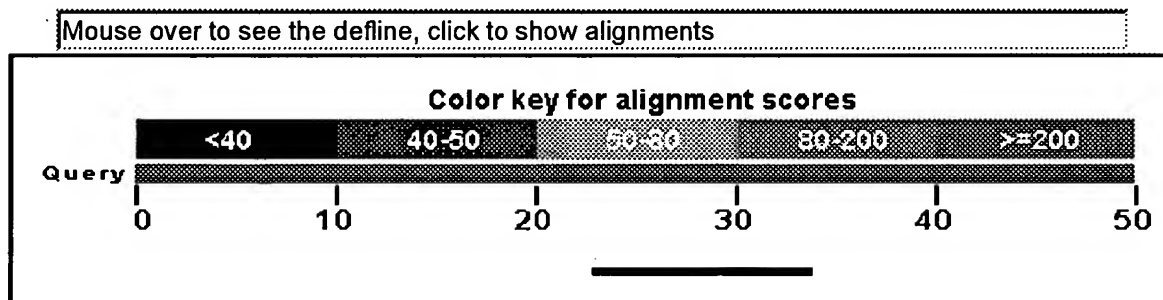protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1139520495-2564-183997461739.BLASTQ4

Database: NCBI Genomic Reference Sequences
           648,380 sequences; 5,833,944,919 total letters

If you have any problems or questions with the results of this search
please refer to the **BLAST FAQs**
Taxonomy reports

Query=
Length=50

Distribution of 2 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments

Color key for alignment scores

| <40 | 40-50 | 50-80 | 80-200 | >=200 |

Query
0   10   20   30   40   50

| | Score | E |
| Sequences producing significant alignments: | (Bits)| Value |

gi|11994090|ref|NC_001666.2| Zea mays chloroplast, complete geno 22.3   1.1

Alignments

| Get selected sequences | Select all | Deselect all |

> gi|11994090|ref|NC_001666.2| Zea mays chloroplast, complete genome
Length=140384

 Score = 22.3 bits (11), Expect = 1.1
 Identities = 11/11 (100%), Gaps = 0/11 (0%)
 Strand=Plus/Plus

```
Query   24      AGGGTGAAGTA     34
                | | | | | | | | | | |
Sbjct   96767   AGGGTGAAGTA     96777
```

```
Score = 22.3 bits (11),  Expect = 1.1
Identities = 11/11 (100%), Gaps = 0/11 (0%)
Strand=Plus/Minus
```

```
Query   24      AGGGTGAAGTA     34
                | | | | | | | | | | |
Sbjct   125970  AGGGTGAAGTA     125960
```

Get selected sequences	Select all	Deselect all

```
Database: NCBI Genomic Reference Sequences
   Posted date:  Feb 7, 2006 12:38 PM
Number of letters in database: 142,297
Number of sequences in database:  2
Lambda      K        H
    1.37     0.711     1.31
Gapped
Lambda      K        H
    1.37     0.711     1.31
Matrix: blastn matrix:1 -3
Gap Penalties: Existence: 5, Extension: 2
Number of Sequences: 2
Number of Hits to DB: 0
Number of extensions: 0
Number of successful extensions: 0
Number of sequences better than 10: 0
Number of HSP's better than 10 without gapping: 0
Number of HSP's gapped: 0
Number of HSP's successfully gapped: 0
Length of query: 50
Length of database: 142297
Length adjustment: 11
Effective length of query: 39
Effective length of database: 142297
Effective search space: 5549583
Effective search space used: 5548725
A: 0
X1: 10 (19.8 bits)
X2: 15 (29.7 bits)
X3: 25 (49.6 bits)
S1: 10 (20.3 bits)
S2: 10 (20.3 bits)
```

NCBI   results of BLAST

BLASTN 2.2.13 [Nov-27-2005]

Reference:
Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman
(1997), "Gapped BLAST and PSI-BLAST: a new generation of
protein database search programs", Nucleic Acids Res. 25:3389-3402.
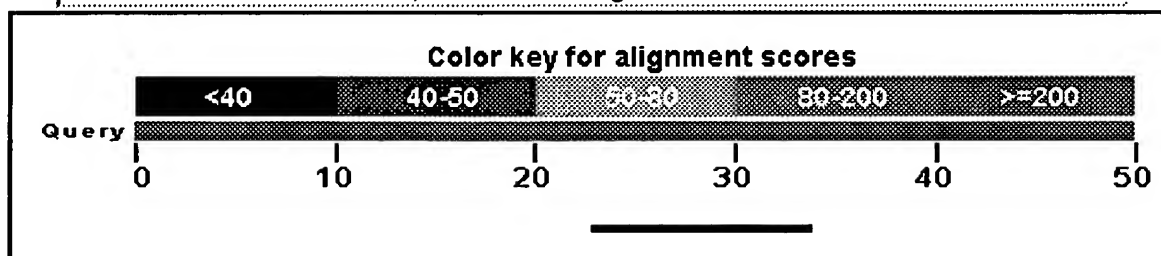
RID: 1139520495-2564-183997461739.BLASTQ4

Database: NCBI Genomic Reference Sequences
          648,380 sequences; 5,833,944,919 total letters

If you have any problems or questions with the results of this search
please refer to the **BLAST FAQs**
Taxonomy reports

Query=
Length=50

Distribution of 2 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments

Color key for alignment scores

| <40 | 40-50 | 50-80 | 80-200 | >=200 |

Query

0   10   20   30   40   50

| | Score | E |
| Sequences producing significant alignments: | (Bits) | Value |

gi|11994090|ref|NC_001666.2| Zea mays chloroplast, complete geno   22.3   1.1

Alignments

| Get selected sequences | Select all | Deselect all |

> gi|11994090|ref|NC_001666.2| Zea mays chloroplast, complete genome
Length=140384

 Score = 22.3 bits (11), Expect = 1.1
 Identities = 11/11 (100%), Gaps = 0/11 (0%)
 Strand=Plus/Plus

```
Query   24      AGGGTGAAGTA   34
                |||||||||||
Sbjct   96767   AGGGTGAAGTA   96777


 Score = 22.3 bits (11),  Expect = 1.1
 Identities = 11/11 (100%), Gaps = 0/11 (0%)
 Strand=Plus/Minus

Query   24      AGGGTGAAGTA   34
                |||||||||||
Sbjct   125970  AGGGTGAAGTA   125960
```

```
|  Get selected sequences  |  | Select all |  | Deselect all |
```

```
  Database: NCBI Genomic Reference Sequences
     Posted date:  Feb 7, 2006 12:38 PM
  Number of letters in database: 142,297
  Number of sequences in database:  2
Lambda      K        H
   1.37     0.711      1.31
Gapped
Lambda      K        H
   1.37     0.711      1.31
Matrix: blastn matrix:1 -3
Gap Penalties: Existence: 5, Extension: 2
Number of Sequences: 2
Number of Hits to DB: 0
Number of extensions: 0
Number of successful extensions: 0
Number of sequences better than 10: 0
Number of HSP's better than 10 without gapping: 0
Number of HSP's gapped: 0
Number of HSP's successfully gapped: 0
Length of query: 50
Length of database: 142297
Length adjustment: 11
Effective length of query: 39
Effective length of database: 142297
Effective search space: 5549583
Effective search space used: 5548725
A: 0
X1: 10 (19.8 bits)
X2: 15 (29.7 bits)
X3: 25 (49.6 bits)
S1: 10 (20.3 bits)
S2: 10 (20.3 bits)
```

NCBI   *results of* **BLAST**

BLASTN 2.2.13 [Nov-27-2005]

<u>**Reference**</u>:
Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman
(1997), "Gapped BLAST and PSI-BLAST: a new generation of
protein database search programs", Nucleic Acids Res. 25:3389-3402.
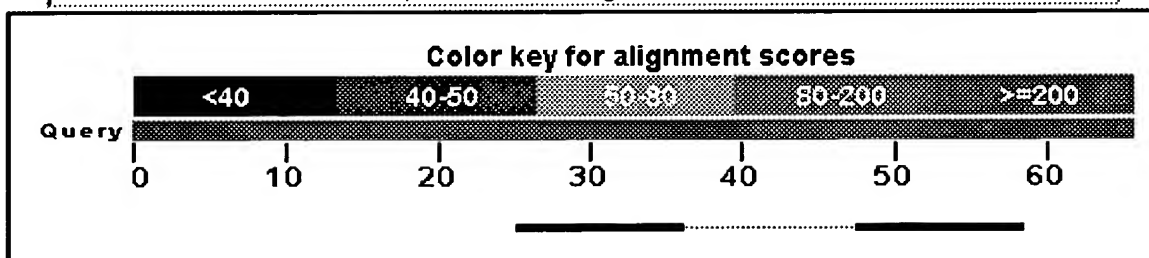
RID: 1139520711-10093-27750649669.BLASTQ4

Database: NCBI Genomic Reference Sequences
           648,380 sequences; 5,833,944,919 total letters

If you have any problems or questions with the results of this search
please refer to the **BLAST FAQs**
<u>Taxonomy reports</u>

Query=
Length=65

Distribution of 3 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments

Color key for alignment scores

| <40 | 40-50 | 50-80 | 80-200 | >=200 |

Query

0   10   20   30   40   50   60

	Score (Bits)	E Value
Sequences producing significant alignments:		
<u>gi|11994090|ref|NC_001666.2|</u> Zea mays chloroplast, complete geno	22.3	1.5

Alignments

| Get selected sequences | Select all | Deselect all |

> gi\|11994090\|ref\|NC_001666.2\| Zea mays chloroplast, complete genome
Length=140384

   Score = 22.3 bits (11),   Expect = 1.5
   Identities = 11/11 (100%), Gaps = 0/11 (0%)
   Strand=Plus/Plus

```
Query  48       GATCTTTTCTC  58
                |||||||||||
Sbjct  44568    GATCTTTTCTC  44578
```

```
 Score = 22.3 bits (11),  Expect = 1.5
 Identities = 11/11 (100%), Gaps = 0/11 (0%)
 Strand=Plus/Plus
```
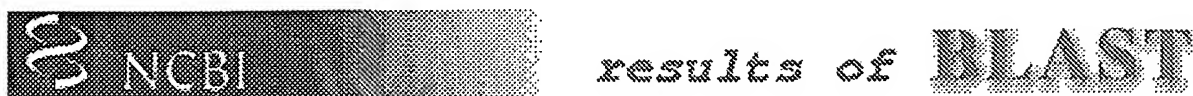
```
Query  26       TCCTCCTCTCT  36
                |||||||||||
Sbjct  83760    TCCTCCTCTCT  83770
```

```
 Score = 22.3 bits (11),  Expect = 1.5
 Identities = 11/11 (100%), Gaps = 0/11 (0%)
 Strand=Plus/Minus
```

```
Query  26       TCCTCCTCTCT  36
                |||||||||||
Sbjct  138977   TCCTCCTCTCT  138967
```

| Get selected sequences | Select all | Deselect all |

```
  Database: NCBI Genomic Reference Sequences
     Posted date:  Feb 7, 2006 12:38 PM
  Number of letters in database: 142,297
  Number of sequences in database:  2
Lambda      K       H
   1.37     0.711     1.31
Gapped
Lambda      K       H
   1.37     0.711     1.31
Matrix: blastn matrix:1 -3
Gap Penalties: Existence: 5, Extension: 2
Number of Sequences: 2
Number of Hits to DB: 0
Number of extensions: 0
Number of successful extensions: 0
Number of sequences better than 10: 0
Number of HSP's better than 10 without gapping: 0
Number of HSP's gapped: 0
Number of HSP's successfully gapped: 0
Length of query: 65
Length of database: 142297
Length adjustment: 11
Effective length of query: 54
Effective length of database: 142297
Effective search space: 7684038
Effective search space used: 7682850
A: 0
X1: 10 (19.8 bits)
X2: 15 (29.7 bits)
X3: 25 (49.6 bits)
S1: 10 (20.3 bits)
```

NCBI   results of BLAST

BLASTN 2.2.13 [Nov-27-2005]

Reference:
Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman
(1997), "Gapped BLAST and PSI-BLAST: a new generation of
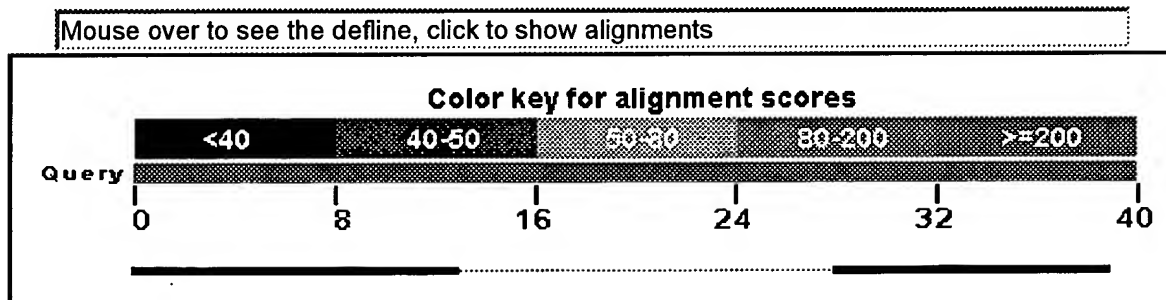protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1139520074-12515-142933253334.BLASTQ4

Database: NCBI Genomic Reference Sequences
             648,380 sequences; 5,833,944,919 total letters

If you have any problems or questions with the results of this search
please refer to the **BLAST FAQs**
Taxonomy reports

Query=
Length=40

Distribution of 3 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments

Color key for alignment scores

| <40 | 40-50 | 50-80 | 80-200 | >=200 |

Query

0   8   16   24   32   40

| | Score | E |
| Sequences producing significant alignments: | (Bits) | Value |

gi|11994090|ref|NC_001666.2| Zea mays chloroplast, complete geno 22.3   0.80

Alignments

Get selected sequences | Select all | Deselect all

> gi|11994090|ref|NC_001666.2| Zea mays chloroplast, complete genome
Length=140384

 Score = 22.3 bits (11), Expect = 0.80
 Identities = 11/11 (100%), Gaps = 0/11 (0%)
 Strand=Plus/Plus

```
Query  3       TCGATCCAAAA  13
               |||||||||||
Sbjct  66973   TCGATCCAAAA  66983
```

```
 Score = 22.3 bits (11),  Expect = 0.80
 Identities = 11/11 (100%), Gaps = 0/11 (0%)
 Strand=Plus/Plus
```

```
Query  1       AATCGATCCAA  11
               |||||||||||
Sbjct  73754   AATCGATCCAA  73764
```

```
 Score = 22.3 bits (11),  Expect = 0.80
 Identities = 11/11 (100%), Gaps = 0/11 (0%)
 Strand=Plus/Plus
```

```
Query  29      TGGAAGAAAGA  39
               |||||||||||
Sbjct  112529  TGGAAGAAAGA  112539
```

Get selected sequences	Select all	Deselect all

```
  Database: NCBI Genomic Reference Sequences
     Posted date:  Feb 7, 2006 12:38 PM
  Number of letters in database: 142,297
  Number of sequences in database:  2
Lambda      K       H
    1.37    0.711    1.31
Gapped
Lambda      K       H
    1.37    0.711    1.31
Matrix: blastn matrix:1 -3
Gap Penalties: Existence: 5, Extension: 2
Number of Sequences: 2
Number of Hits to DB: 0
Number of extensions: 0
Number of successful extensions: 0
Number of sequences better than 10: 0
Number of HSP's better than 10 without gapping: 0
Number of HSP's gapped: 0
Number of HSP's successfully gapped: 0
Length of query: 40
Length of database: 142297
Length adjustment: 11
Effective length of query: 29
Effective length of database: 142297
Effective search space: 4126613
Effective search space used: 4125975
A: 0
X1: 10 (19.8 bits)
X2: 15 (29.7 bits)
X3: 25 (49.6 bits)
S1: 10 (20.3 bits)
```
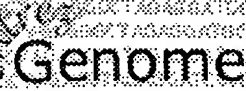
All Databases   PubMed   Nucleotide   Protein   Genome   Structure   PMC   Taxonomy   Book

Search [Genome ▼] for [   ] [Go] [Clear]

Limits   Preview/Index   History   Clipboard   Details

Display [Overview ▼]   Show [20 ▼] [Send to ▼]

All: 1

Genome > *Eukaryota* > *Zea mays chloroplast, complete genome*

Lineage: Eukaryota ; Viridiplantae ; Streptophyta ; Streptophytina ; Embryophyta ; Tracheophyta ; Euph
Magnoliophyta ; Liliopsida ; commelinids ; Poales ; Poaceae ; PACCAD clade ; Panicoideae ; Andropog

Genome Info:	Feature table:	BLAST homologs:	Links:	Reviev
Refseq: NC_001666	Proteins: 111	COG	Genome Project	Public
GenBank: X86563	Structural RNAs: 47	3D Structure	Refseq FTP	Refse
Length: **140,384 nt**	Genes: 155	TaxMap	GenBank FTP	Seq.S
GC Content: **38%**	Others: 153	TaxPlot	BLAST	Seque
Topology: **circular**	Total: **466**	GenePlot	TraceAssembly	Comp
Molecule: **DNA**	Contigs: 1	gMap	CDD	Organ
Gen.Code: 1			Other genomes for species	

Gene Classification based on COG functional categories   Search gene, GeneID or locus_tag:

Zoom
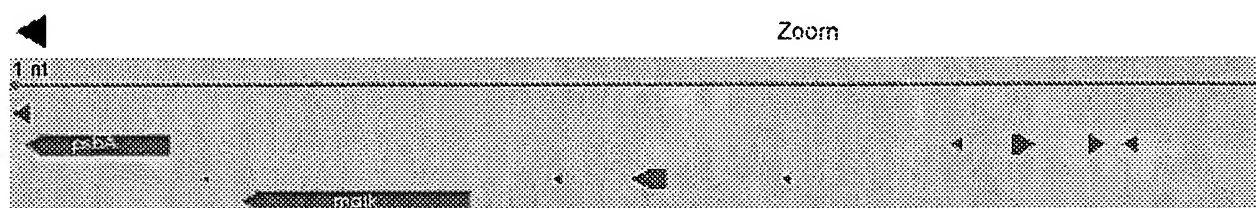
Comment and suggestions to: [info@ncbi.nlm.nih.gov]

Display [Overview ▼]   Show [20 ▼] [Send to ▼]

Feb 6 2006 06:28.59

NCBI   results of BLAST

BLASTN 2.2.13 [Nov-27-2005]

Reference:
Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman
(1997), "Gapped BLAST and PSI-BLAST: a new generation of
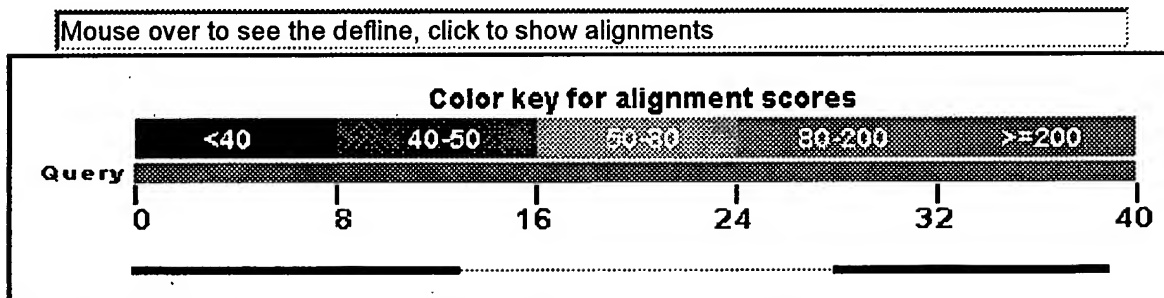protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1139520074-12515-142933253334.BLASTQ4

Database: NCBI Genomic Reference Sequences
       648,380 sequences; 5,833,944,919 total letters

If you have any problems or questions with the results of this search
please refer to the **BLAST FAQs**
Taxonomy reports

Query=
Length=40

Distribution of 3 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments

Color key for alignment scores

| <40 | 40-50 | 50-80 | 80-200 | >=200 |

Query

0   8   16   24   32   40

	Score (Bits)	E Value
Sequences producing significant alignments:		
gi|11994090|ref|NC_001666.2| Zea mays chloroplast, complete geno	22.3	0.80

Alignments

| Get selected sequences | Select all | Deselect all |

> gi\|11994090\|ref\|NC_001666.2\| Zea mays chloroplast, complete genome
Length=140384

  Score = 22.3 bits (11), Expect = 0.80
  Identities = 11/11 (100%), Gaps = 0/11 (0%)
  Strand=Plus/Plus

```
Query  3       TCGATCCAAAA  13
               |||||||||||
Sbjct  66973   TCGATCCAAAA  66983
```

```
 Score = 22.3 bits (11),  Expect = 0.80
 Identities = 11/11 (100%), Gaps = 0/11 (0%)
 Strand=Plus/Plus
```

```
Query  1       AATCGATCCAA  11
               |||||||||||
Sbjct  73754   AATCGATCCAA  73764
```

```
 Score = 22.3 bits (11),  Expect = 0.80
 Identities = 11/11 (100%), Gaps = 0/11 (0%)
 Strand=Plus/Plus
```

```
Query  29      TGGAAGAAAGA  39
               |||||||||||
Sbjct  112529  TGGAAGAAAGA  112539
```

| Get selected sequences | Select all | Deselect all |

```
  Database: NCBI Genomic Reference Sequences
    Posted date:  Feb 7, 2006 12:38 PM
  Number of letters in database: 142,297
  Number of sequences in database:  2
Lambda     K       H
    1.37    0.711    1.31
Gapped
Lambda     K       H
    1.37    0.711    1.31
Matrix: blastn matrix:1 -3
Gap Penalties: Existence: 5, Extension: 2
Number of Sequences: 2
Number of Hits to DB: 0
Number of extensions: 0
Number of successful extensions: 0
Number of sequences better than 10: 0
Number of HSP's better than 10 without gapping: 0
Number of HSP's gapped: 0
Number of HSP's successfully gapped: 0
Length of query: 40
Length of database: 142297
Length adjustment: 11
Effective length of query: 29
Effective length of database: 142297
Effective search space: 4126613
Effective search space used: 4125975
A: 0
X1: 10 (19.8 bits)
X2: 15 (29.7 bits)
X3: 25 (49.6 bits)
S1: 10 (20.3 bits)
```